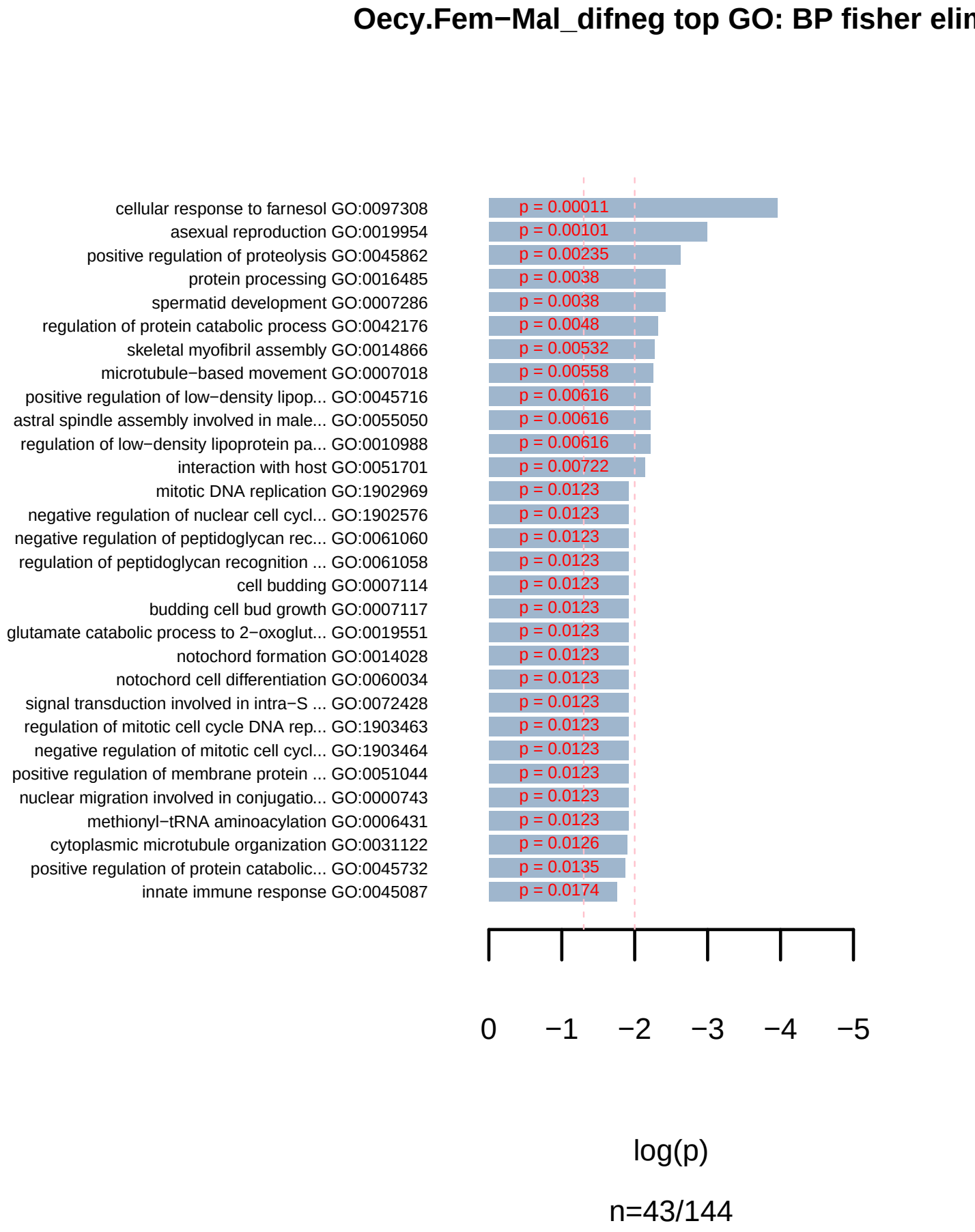
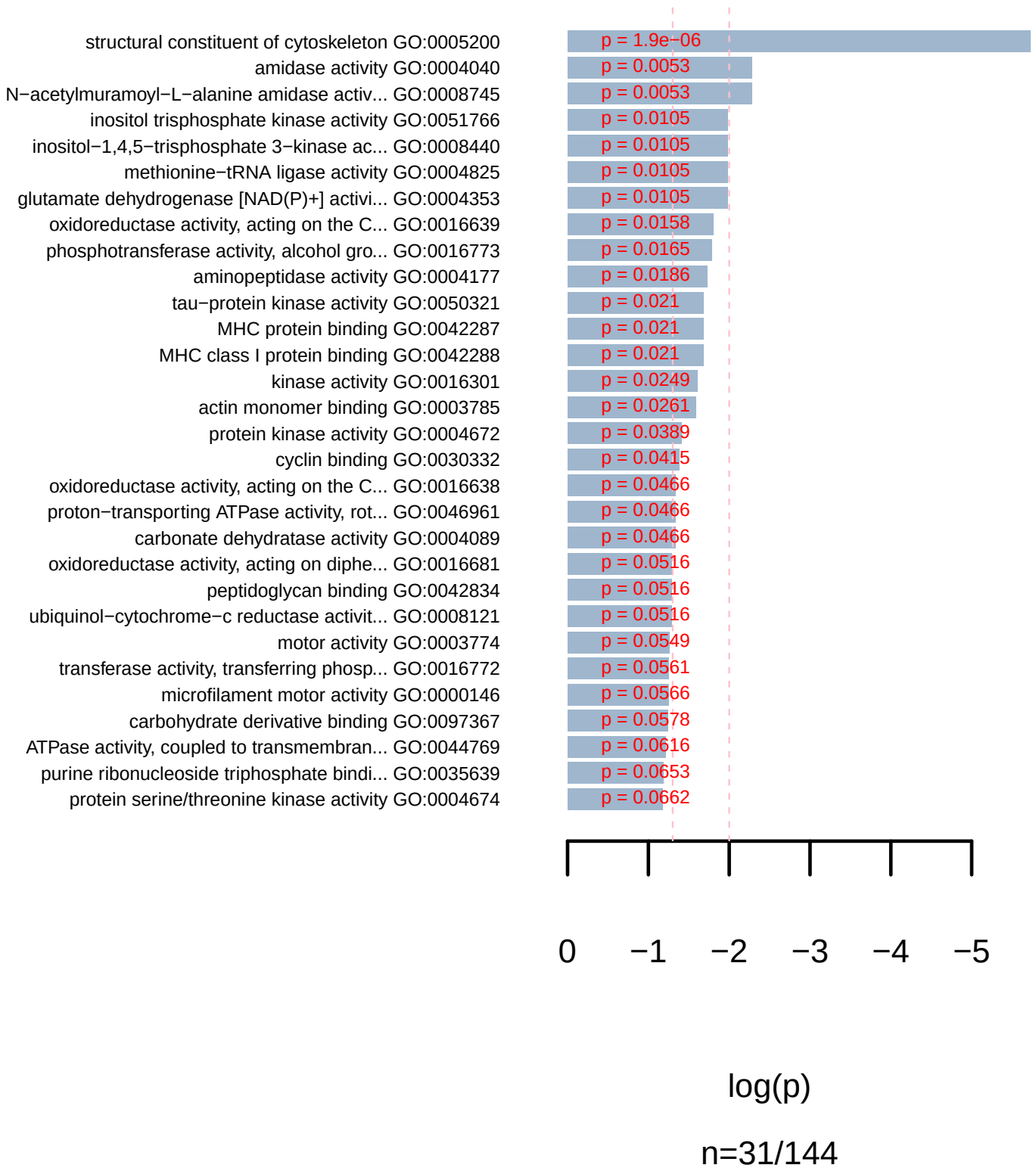
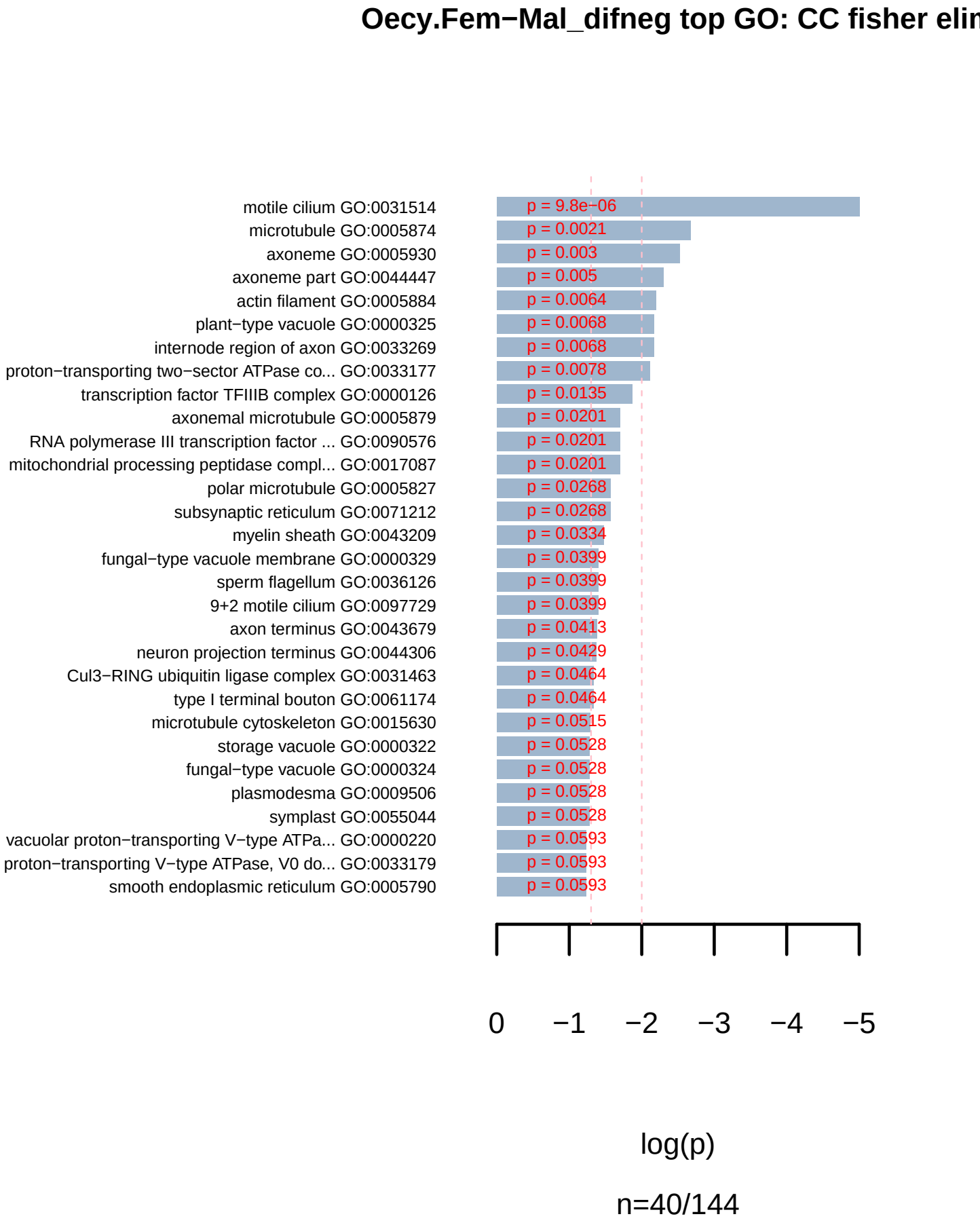

Oecy.Fem−Mal_difneg top GO: BP fisher elim
cellular response to farnesol GO:0097308
asexual reproduction GO:0019954
positive regulation of proteolysis GO:0045862
protein processing GO:0016485
spermatid development GO:0007286
regulation of protein catabolic process GO:0042176
skeletal myofibril assembly GO:0014866
microtubule−based movement GO:0007018
positive regulation of low−density lipop... GO:0045716
astral spindle assembly involved in male... GO:0055050
regulation of low−density lipoprotein pa... GO:0010988
interaction with host GO:0051701
mitotic DNA replication GO:1902969
negative regulation of nuclear cell cycl... GO:1902576
negative regulation of peptidoglycan rec... GO:0061060
regulation of peptidoglycan recognition ... GO:0061058
cell budding GO:0007114
budding cell bud growth GO:0007117
glutamate catabolic process to 2−oxoglut... GO:0019551
notochord formation GO:0014028
notochord cell differentiation GO:0060034
signal transduction involved in intra−S ... GO:0072428
regulation of mitotic cell cycle DNA rep... GO:1903463
negative regulation of mitotic cell cycl... GO:1903464
positive regulation of membrane protein ... GO:0051044
nuclear migration involved in conjugatio... GO:0000743
methionyl−tRNA aminoacylation GO:0006431
cytoplasmic microtubule organization GO:0031122
positive regulation of protein catabolic... GO:0045732
innate immune response GO:0045087
p = 0.00011
p = 0.00101
p = 0.00235
p = 0.0038
p = 0.0038
p = 0.0048
p = 0.00532
p = 0.00558
p = 0.00616
p = 0.00616
p = 0.00616
p = 0.00722
p = 0.0123
p = 0.0123
p = 0.0123
p = 0.0123
p = 0.0123
p = 0.0123
p = 0.0123
p = 0.0123
p = 0.0123
p = 0.0123
p = 0.0123
p = 0.0123
p = 0.0123
p = 0.0123
p = 0.0123
p = 0.0123
p = 0.0126
p = 0.0135
p = 0.0174
0
−1
−2
−3
−4
−5
log(p)
n=43/144

Oecy.Fem−Mal_difneg top GO: MF fisher elim




Oecy.Fem−Mal_difneg top GO: CC fisher elim
motile cilium GO:0031514
microtubule GO:0005874
axoneme GO:0005930
axoneme part GO:0044447
actin filament GO:0005884
plant−type vacuole GO:0000325
internode region of axon GO:0033269
proton−transporting two−sector ATPase co... GO:0033177
transcription factor TFIIIB complex GO:0000126
axonemal microtubule GO:0005879
RNA polymerase III transcription factor ... GO:0090576
mitochondrial processing peptidase compl... GO:0017087
polar microtubule GO:0005827
subsynaptic reticulum GO:0071212
myelin sheath GO:0043209
fungal−type vacuole membrane GO:0000329
sperm flagellum GO:0036126
9+2 motile cilium GO:0097729
axon terminus GO:0043679
neuron projection terminus GO:0044306
Cul3−RING ubiquitin ligase complex GO:0031463
type I terminal bouton GO:0061174
microtubule cytoskeleton GO:0015630
storage vacuole GO:0000322
fungal−type vacuole GO:0000324
plasmodesma GO:0009506
symplast GO:0055044
vacuolar proton−transporting V−type ATPa... GO:0000220
proton−transporting V−type ATPase, V0 do... GO:0033179
smooth endoplasmic reticulum GO:0005790
p = 9.8e−06
p = 0.0021
p = 0.003
p = 0.005
p = 0.0064
p = 0.0068
p = 0.0068
p = 0.0078
p = 0.0135
p = 0.0201
p = 0.0201
p = 0.0201
p = 0.0268
p = 0.0268
p = 0.0334
p = 0.0399
p = 0.0399
p = 0.0399
p = 0.0413
p = 0.0429
p = 0.0464
p = 0.0464
p = 0.0515
p = 0.0528
p = 0.0528
p = 0.0528
p = 0.0528
p = 0.0593
p = 0.0593
p = 0.0593
0
−1
−2
−3
−4
−5
log(p)
n=40/144